

SEQUENCE LISTING

<110> DEKISHIMA, YASUKATA
 KAWABATA, HIROSHI
 HIRAOKA, HIROTOSHI
 UEDA, MAKOTO
 UEHARA, HISATOSHI

<120> METHOD FOR PRODUCING ALCOHOL AND CARBOXYLIC ACID
 HAVING OPTICAL ACTIVITY

<130> P30416

<140> 10/588,286

<141> 2006-08-04

<150> PCT/JP05/02093

<151> 2005-02-04

<150> JP 027815/2004

<151> 2004-02-04

<150> JP 147023/2004

<151> 2004-04-13

<160> 13

<170> PatentIn Ver. 3.3

<210> 1

<211> 345

<212> PRT

<213> Issatchenkia scutulata

<400> 1

Met	Ser	Asn	Lys	Thr	Val	Leu	Val	Thr	Gly	Ala	Thr	Gly	Phe	Ile	Ala
1					5				10					15	
Leu	His	Ile	Ile	Asp	Asn	Leu	Leu	Ser	Lys	Gly	Tyr	Ser	Val	Ile	Gly
			20					25					30		
Thr	Ala	Arg	Ser	Gln	Ser	Lys	Tyr	Gln	Pro	Ile	Leu	Asp	Ala	Phe	Lys
		35					40					45			
Lys	Lys	Tyr	Pro	Asp	Ala	Asn	Leu	Thr	Phe	Glu	Val	Val	Pro	Asp	Ile
	50					55					60				
Ser	Thr	Glu	Asn	Ala	Phe	Asp	Asp	Val	Leu	Lys	Lys	His	Pro	Glu	Ile
65				70						75				80	
Thr	Ala	Val	Leu	His	Thr	Ala	Ser	Pro	Phe	Ser	Phe	Gly	Leu	Asn	Lys
				85					90					95	
Asp	Leu	Lys	Glu	Ala	Tyr	Leu	Lys	Pro	Ala	Val	Asp	Gly	Thr	Leu	Asn
		100						105					110		
Ile	Leu	Lys	Ala	Ile	Glu	Lys	Tyr	Ala	Pro	Gln	Val	Thr	Lys	Val	Val
		115					120					125			

Ile Thr Ser Ser Tyr Ala Ala Ile Met Thr Gly Asn Pro Ser His Val
 130 135 140
 His Thr Ser Glu Thr Trp Asn Pro Ile Asn Trp Glu Asn Asp Val Lys
 145 150 155 160
 Asn Glu Tyr Phe Ala Tyr Ile Ala Ser Lys Thr Tyr Ala Glu Lys Ala
 165 170 175
 Ala Arg Asp Phe Val Lys Glu His Lys Val Asn Phe Lys Leu Ala Thr
 180 185 190
 Val Asn Pro Pro Tyr Val Leu Gly Pro Gln Leu Phe Asp Phe Ser Val
 195 200 205
 Gly Pro Val Leu Asn Thr Ser Asn Gln Leu Ile Thr Asp Ala Thr Lys
 210 215 220
 Ile Asp Lys Asn Ser Thr Lys Pro Glu Leu Gly Thr Pro Ala Leu Ala
 225 230 235 240
 Val Asp Val Arg Asp Val Ala Ala Phe His Val Leu Pro Leu Glu Asp
 245 250 255
 Asp Lys Val Ala Ser Glu Arg Leu Phe Ile Val Ala Gly Pro Ala Val
 260 265 270
 Val Gln Thr Phe Leu Asn Ile Ile Asn Glu Asn Ile Pro Glu Leu Lys
 275 280 285
 Gly Lys Val Ala Leu Gly Asp Pro Ala Ser Glu Lys Glu Leu Ile Glu
 290 295 300
 Lys His Thr Asp Lys Tyr Asp Leu Thr Asn Leu His Asn Val Ile Gly
 305 310 315 320
 Lys Tyr Asp Phe Ile Pro Val Glu Lys Ser Val Val Asp Val Leu Glu
 325 330 335
 Gln Tyr Tyr Lys Ile Asn Lys Ile Asp
 340 345

<210> 2

<211> 1038

<212> DNA

<213> Issatchenkia scutulata

<400> 2

atgtcgaaca aaacagttct agtcaccggg gctaccggtt ttattgcact acacatcatt 60
 gataatttat tgtctaaggg ttattccggt attggtacag ctagatccca atctaaatat 120
 caaccaatcc ttgatgcttt caagaaaaaa taccctgatg caaatttgac ttttgaagtt 180
 gtccctgaca tctccactga aaacgcattc gatgatgttt tgaagaagca tccagaaatt 240
 actgctgtcc ttcacacagc atctccattc tcttttggtt tgaacaagga tctgaaggaa 300
 gcatatttga agcctgccgt tgatggtact ttgaatattc tcaaggcaat tgagaagtat 360
 gcaccacagg ttactaaagt tgttatcaca tcttcttatg ctgcaattat gacaggtaat 420
 ccaagtcatg tccacaccag tgaaacctgg aaccctaatta attgggaaaa cgatgtgaag 480

```

aatgaataact ttgcatatat tgcctccaag acgtatgctg aaaaagctgc gagagatttt 540
gtcaaggagc ataaggtcaa tttcaagtta gcaactgtta acccaccata cgttctgggt 600
ccacaattat ttgacttctc agttgggtcca gtcttgaaca cttccaacca attgatcacg 660
gatgcgacta aaattgataa gaactctact aagccggaat taggtacacc agcttttagca 720
gtcgtatgtta gagatgttgc tgcgttccat gttttacat tggaagatga taaagttgca 780
agtgaagat tattttattgt tgcgtgtcca gcagttgttc aaacattctt aaacatcatc 840
aacgagaaca ttccagaact taaaggtaag gttgccctag gagatccagc ttcagagaag 900
gagttgattg aaaagcacac agataagtat gatttgacaa atcttcacaa cgttattggt 960
aaatatgatt tcattccagt tgaaaagtcc gttgtcgacg tcttagaaca atattacaaa 1020
atcaataaaaa ttgattag 1038

```

<210> 3

<211> 344

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 3

```

Met Ser Asn Thr Val Leu Val Ser Gly Ala Ser Gly Phe Ile Ala Leu
  1              5              10              15

His Ile Leu Ser Gln Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr
      20              25              30

Val Arg Ser His Glu Lys Glu Ala Lys Leu Leu Arg Gln Phe Gln His
      35              40              45

Asn Pro Asn Leu Thr Leu Glu Ile Val Pro Asp Ile Ser His Pro Asn
  50              55              60

Ala Phe Asp Lys Val Leu Gln Lys Arg Gly Arg Glu Ile Arg Tyr Val
  65              70              75              80

Leu His Thr Ala Ser Pro Phe His Tyr Asp Thr Thr Glu Tyr Glu Lys
      85              90              95

Asp Leu Leu Ile Pro Ala Leu Glu Gly Thr Lys Asn Ile Leu Asn Ser
 100              105              110

Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Arg Val Val Val Thr Ser
 115              120              125

Ser Cys Thr Ala Ile Ile Thr Leu Ala Lys Met Asp Asp Pro Ser Val
 130              135              140

Val Phe Thr Glu Glu Ser Trp Asn Glu Ala Thr Trp Glu Ser Cys Gln
 145              150              155              160

Ile Asp Gly Ile Asn Ala Tyr Phe Ala Ser Lys Lys Phe Ala Glu Lys
      165              170              175

Ala Ala Trp Glu Phe Thr Lys Glu Asn Glu Asp His Ile Lys Phe Lys
      180              185              190

Leu Thr Thr Val Asn Pro Ser Leu Leu Phe Gly Pro Gln Leu Phe Asp
 195              200              205

```

Glu Asp Val His Gly His Leu Asn Thr Ser Cys Glu Met Ile Asn Gly
 210 215 220

Leu Ile His Thr Pro Val Asn Ala Ser Val Pro Asp Phe His Ser Ile
 225 230 235 240

Phe Ile Asp Val Arg Asp Val Ala Leu Ala His Leu Tyr Ala Phe Gln
 245 250 255

Lys Glu Asn Thr Ala Gly Lys Arg Leu Val Val Thr Asn Gly Lys Phe
 260 265 270

Gly Asn Gln Asp Ile Leu Asp Ile Leu Asn Glu Asp Phe Pro Gln Leu
 275 280 285

Arg Gly Leu Ile Pro Leu Gly Lys Pro Gly Thr Gly Asp Gln Val Ile
 290 295 300

Asp Arg Gly Ser Thr Thr Asp Asn Ser Ala Thr Arg Lys Ile Leu Gly
 305 310 315 320

Phe Glu Phe Arg Ser Leu His Glu Ser Val His Asp Thr Ala Ala Gln
 325 330 335

Ile Leu Lys Lys Glu Asn Arg Leu
 340

<210> 4

<211> 18

<212> PRT

<213> Issatchenkia scutulata

<400> 4

Arg Asn Lys Thr Val Leu Val Thr Gly Ala Thr Gly Phe Ile Ala Leu
 1 5 10 15

Asp Ile

<210> 5

<211> 15

<212> PRT

<213> Issatchenkia scutulata

<400> 5

Val Val Ile Thr Ser Ser Tyr Ala Ala Ile Met Thr Gly Asn Pro
 1 5 10 15

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (3)
<223> Inosine

<220>
<221> modified_base
<222> (6)
<223> Inosine

<220>
<221> modified_base
<222> (15)
<223> Inosine

<220>
<221> modified_base
<222> (18)
<223> Inosine

<400> 6
acnggnttya thgcnytn ga yat

23

<210> 7
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (6)
<223> Inosine

<220>
<221> modified_base
<222> (9)
<223> Inosine

<220>
<221> modified_base
<222> (18)
<223> Inosine

<220>
<221> modified_base
<222> (21)
<223> Inosine

<400> 7
ggrttncng tcatdatngc ngcrta

26

<210> 8
<211> 341
<212> DNA
<213> Issatchenkia scutulata

<400> 8
cattgataat ttattgtcta agggttattc cgttattggt acagctagat cccaatctaa 60
atatcaacca atccttgatg ctttcaagaa aaaataccct gatgcaaatt tgacttttga 120
agttgtccct gacatctcca ctgaaaacgc attcgatgat gttttgaaga agcatccaga 180
aattactgct gtccttcaca cagcatctcc attctctttt ggtttgaaca aggatctgaa 240
ggaagcatat ttgaagcctg ccgttgatgg tactttgaat attctcaagg caattgagaa 300
gtatgcacca caggttacta aagttgttat cacatcttct t 341

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 9
agggttattc cgttattggt acagctag

28

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 10
gagaatggag atgctgtgtg aaggacagca g

31

<210> 11
<211> 1212
<212> DNA
<213> Issatchenkia scutulata

<220>
<221> CDS
<222> (55)..(1089)

<400> 11
tcatgacctg tccactgata gcatcatacc aaacatatc agtatattgt aaca atg 57
Met
1

tcg aac aaa aca gtt cta gtc acc ggg gct acc ggt ttt att gca cta	105
Ser Asn Lys Thr Val Leu Val Thr Gly Ala Thr Gly Phe Ile Ala Leu	
5 10 15	
cac atc att gat aat tta ttg tct aag ggt tat tcc gtt att ggt aca	153
His Ile Ile Asp Asn Leu Leu Ser Lys Gly Tyr Ser Val Ile Gly Thr	
20 25 30	
gct aga tcc caa tct aaa tat caa cca atc ctt gat gct ttc aag aaa	201
Ala Arg Ser Gln Ser Lys Tyr Gln Pro Ile Leu Asp Ala Phe Lys Lys	
35 40 45	
aaa tac cct gat gca aat ttg act ttt gaa gtt gtc cct gac atc tcc	249
Lys Tyr Pro Asp Ala Asn Leu Thr Phe Glu Val Val Pro Asp Ile Ser	
50 55 60 65	
act gaa aac gca ttc gat gat gtt ttg aag aag cat cca gaa att act	297
Thr Glu Asn Ala Phe Asp Asp Val Leu Lys Lys His Pro Glu Ile Thr	
70 75 80	
gct gtc ctt cac aca gca tct cca ttc tct ttt ggt ttg aac aag gat	345
Ala Val Leu His Thr Ala Ser Pro Phe Ser Phe Gly Leu Asn Lys Asp	
85 90 95	
ctg aag gaa gca tat ttg aag cct gcc gtt gat ggt act ttg aat att	393
Leu Lys Glu Ala Tyr Leu Lys Pro Ala Val Asp Gly Thr Leu Asn Ile	
100 105 110	
ctc aag gca att gag aag tat gca cca cag gtt act aaa gtt gtt atc	441
Leu Lys Ala Ile Glu Lys Tyr Ala Pro Gln Val Thr Lys Val Val Ile	
115 120 125	
aca tct tct tat gct gca att atg aca ggt aat cca agt cat gtc cac	489
Thr Ser Ser Tyr Ala Ala Ile Met Thr Gly Asn Pro Ser His Val His	
130 135 140 145	
acc agt gaa acc tgg aac cca att aat tgg gaa aac gat gtg aag aat	537
Thr Ser Glu Thr Trp Asn Pro Ile Asn Trp Glu Asn Asp Val Lys Asn	
150 155 160	
gaa tac ttt gca tat att gcc tcc aag acg tat gct gaa aaa gct gcg	585
Glu Tyr Phe Ala Tyr Ile Ala Ser Lys Thr Tyr Ala Glu Lys Ala Ala	
165 170 175	
aga gat ttt gtc aag gag cat aag gtc aat ttc aag tta gca act gtt	633
Arg Asp Phe Val Lys Glu His Lys Val Asn Phe Lys Leu Ala Thr Val	
180 185 190	
aac cca cca tac gtt ctg ggt cca caa tta ttt gac ttc tca gtt ggt	681
Asn Pro Pro Tyr Val Leu Gly Pro Gln Leu Phe Asp Phe Ser Val Gly	
195 200 205	
cca gtc ttg aac act tcc aac caa ttg atc acg gat gcg act aaa att	729
Pro Val Leu Asn Thr Ser Asn Gln Leu Ile Thr Asp Ala Thr Lys Ile	
210 215 220 225	

gat aag aac tct act aag ccg gaa tta ggt aca cca gct tta gca gtc	777
Asp Lys Asn Ser Thr Lys Pro Glu Leu Gly Thr Pro Ala Leu Ala Val	
230 235 240	
gat gtt aga gat gtt gct gcg ttc cat gtt tta cca ttg gaa gat gat	825
Asp Val Arg Asp Val Ala Ala Phe His Val Leu Pro Leu Glu Asp Asp	
245 250 255	
aaa gtt gca agt gaa aga tta ttt att gtt gct ggt cca gca gtt gtt	873
Lys Val Ala Ser Glu Arg Leu Phe Ile Val Ala Gly Pro Ala Val Val	
260 265 270	
caa aca ttc tta aac atc atc aac gag aac att cca gaa ctt aaa ggt	921
Gln Thr Phe Leu Asn Ile Ile Asn Glu Asn Ile Pro Glu Leu Lys Gly	
275 280 285	
aag gtt gcc cta gga gat cca gct tca gag aag gag ttg att gaa aag	969
Lys Val Ala Leu Gly Asp Pro Ala Ser Glu Lys Glu Leu Ile Glu Lys	
290 295 300 305	
cac aca gat aag tat gat ttg aca aat ctt cac aac gtt att ggt aaa	1017
His Thr Asp Lys Tyr Asp Leu Thr Asn Leu His Asn Val Ile Gly Lys	
310 315 320	
tat gat ttc att cca gtt gaa aag tcc gtt gtc gac gtc tta gaa caa	1065
Tyr Asp Phe Ile Pro Val Glu Lys Ser Val Val Asp Val Leu Glu Gln	
325 330 335	
tat tac aaa atc aat aaa att gat tagtttatat agaaaatttt atagctaaag	1119
Tyr Tyr Lys Ile Asn Lys Ile Asp	
340 345	
gccgaatcaa cttctttctt cctcttcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1179
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa	1212

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 12	
cggaattcat gtcgaacaaa acagttctag tcacc	35

<210> 13
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 13

gctctagatt aatcaatttt attgattttg taatattg

38